Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

Claims 1 and 3 through 24 previously cancelled

2. Currently canceled

Please add the following new claims:

25. (newly added) A method for identifying a compound that inhibits binding of NF-kappaB essential modulator (NEMO) polypeptide to a polypeptide encoded by a putative tumor suppressor gene associated with familial cylindromatosis (CYLD) comprising:

(a) mixing a test compound with a NEMO polypeptide that is capable of binding a CYLD polypeptide comprising amino acids 1 through 956 of SEQ ID NO:4, wherein the NEMO polypeptide is selected from the group consisting of

(i) a NEMO polypeptide comprising amino acids 287 through 419 of SEQ ID NO:2;

(ii) fragments of the NEMO polypeptide of (i), and

(iii) variants of the NEMO polypeptides of (i) and (ii) that are at least 80 % identical to SEQ ID NO:2;

and a binding partner of the NEMO polypeptide, which binding partner is capable of binding a NEMO polypeptide of (i), and is selected from the group consisting of

(iv) a CYLD polypeptide comprising amino acids 1 through 956 of SEQ ID NO:4

(v) fragments of the CYLD polypeptide of (iv), and

(vi) variants of the CYLD polypeptides of (iv) and (v) that are at least 80 % identical to SEQ ID NO:4,

and

(b) determining whether the test compound inhibits the binding activity of the

NEMO and CYLD polypeptides,
wherein inhibition of binding of NEMO to CYLD by at least 50% indicates that the compound is an antagonist of NEMO activity in CD40 Signaling.

26. (newly added) The method according to claim 25, wherein the NEMO polypeptide is selected from the group consisting of:

(a) a NEMO polypeptide comprising amino acids 300 through 419 of SEQ ID NO:2;

(b) a fragment of a NEMO polypeptide comprising amino acids x through y of SEQ ID NO:2, wherein x is selected from the group consisting of 386, 385, 384, 383, 382, 381, 380, 379, 378 and 377, and y is selected from the group consisting of 409, 410, 411, 412, 413, 414, 415, 416, 417, 418 and 419.

27. (newly added) The method of claim 26, wherein the NEMO polypeptide is selected from the group consisting of:
(a) a NEMO polypeptide comprising amino acids 300 through 419 of SEQ ID NO:2; and
(b) a NEMO polypeptide comprising amino acids 387 through 419 of SEQ ID NO:2.

28. (newly added) The method of claim 25, wherein the method utilizes a homogeneous assay format.

29. (newly added) The method of claim 26, wherein the method utilizes a homogeneous assay format.

30. (newly added) The method of claim 27, wherein the method utilizes a homogeneous assay format.

31. (newly added) The method of claim 28, wherein homogeneous assay format is selected from a group consisting of fluorescence resonance energy transfer, fluorescence polarization, time-resolved fluorescence resonance energy transfer,

scintillation proximity assays, reporter gene assays, fluorescence quenched enzyme substrate, chromogenic enzyme substrate and electrochemiluminescence assays.

32. (newly added) The method of claim 29, wherein homogeneous assay format is selected from a group consisting of fluorescence resonance energy transfer, fluorescence polarization, time-resolved fluorescence resonance energy transfer, scintillation proximity assays, reporter gene assays, fluorescence quenched enzyme substrate, chromogenic enzyme substrate and electrochemiluminescence assays.

33. (newly added) The method of claim 30, wherein homogeneous assay format is selected from a group consisting of fluorescence resonance energy transfer, fluorescence polarization, time-resolved fluorescence resonance energy transfer, scintillation proximity assays, reporter gene assays, fluorescence quenched enzyme substrate, chromogenic enzyme substrate and electrochemiluminescence assays.

34. (newly added) A method for identifying a compound that inhibits binding of NEMO to CYLD comprising:

(a) mixing a test compound with a NEMO polypeptide that is capable of binding a CYLD polypeptide consisting essentially of amino acids 1 through 956 of SEQ ID NO:4, wherein the NEMO polypeptide selected from the group consisting of

(i) a NEMO polypeptide consisting essentially of amino acids 287 through 419 of SEQ ID NO:2;

(ii) fragments of the NEMO polypeptide of (i), and

(iii) variants of the NEMO polypeptides of (i) and (ii) that are at least 80 % identical to SEQ ID NO:2;

and a binding partner of the NEMO polypeptide, which binding partner is capable of binding a NEMO polypeptide of (i), and is selected from the group consisting of

(iv) a CYLD polypeptide consisting essentially of amino acids 1 through 956 of SEQ ID NO:4

(v) fragments of the CYLD polypeptide of (iv), and

(vi) variants of the CYLD polypeptides of (iv) and (v) that are at least 80

% identical to SEQ ID NO:4,

and

(b) determining whether the test compound inhibits the binding of the NEMO polypeptide to the CYLD polypeptide,

wherein inhibition of the binding of the NEMO polypeptide to the CYLD polypeptide by at least 50% indicates that the compound is an antagonist of NEMO activity in CD40 signaling.

35. (newly added) The method according to claim 25, wherein the NEMO polypeptide is selected from the group consisting of:

(a) a NEMO polypeptide consisting essentially of amino acids 300 through 419 of SEQ ID NO:2;

(b) a fragment of a NEMO polypeptide consisting essentially of amino acids x through y of SEQ ID NO:2, wherein x is selected from the group consisting of 386, 385, 384, 383, 382, 381, 380, 379, 378 and 377, and y is selected from the group consisting of 409, 410, 411, 412, 413, 414, 415, 416, 417, 418 and 419.

36. (newly added) The method of claim 34, wherein the method utilizes a homogeneous assay format.

37. (newly added) The method of claim 35, wherein the method utilizes a homogeneous assay format.

38. (newly added) The method of claim 36, wherein homogeneous assay format is selected from a group consisting of fluorescence resonance energy transfer, fluorescence polarization, time-resolved fluorescence resonance energy transfer, scintillation proximity assays, reporter gene assays, fluorescence quenched enzyme substrate, chromogenic enzyme substrate and electrochemiluminescence assays.

39. (newly added) The method of claim 37, wherein homogeneous assay format is selected from a group consisting of fluorescence resonance energy transfer,

fluorescence polarization, time-resolved fluorescence resonance energy transfer, scintillation proximity assays, reporter gene assays, fluorescence quenched enzyme substrate, chromogenic enzyme substrate and electrochemiluminescence assays.